

GenCore version 5.1.4\_p5\_4578  
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OM protein - protein search, using sw model

Run on: March 17, 2003, 16:38:32 ; Search time 19 Seconds  
(without alignments)  
1315.524 Million cell updates/sec

Title: US-09-840-243B-11  
Perfect score: 1341  
Sequence: 1 MELTPAEDLIQTQTPASE.....VIENHILKLFQSNLVPADPE 260

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 73:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. NO. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	219.5	16.4	426	2	AE2149	hypothetical prote
2	214	16.0	2039	2	T15347	ankyrin-related un
3	207.5	15.5	1031	2	T43458	hypothetical prote
4	202.5	15.1	3924	2	S37431	ankyrin 2, neurona
5	193	14.4	4377	2	A55575	ankyrin 3, long sp
6	189	14.1	1001	2	S30385	G9a protein - huma
7	188.5	14.1	1765	2	T42714	ankyrin 3, splice
8	188.5	14.1	1940	2	T42715	ankyrin 3, splice
9	188.5	14.1	1943	2	T42713	ankyrin 3, splice
10	188.5	14.1	1961	2	T42716	ankyrin 1, erythro
11	184	13.7	1881	1	SJHUK	ankyrin, erythrocy
12	183	13.6	1848	2	S37771	ankyrin - mouse
13	183	13.6	1862	2	T49502	ankyrin 1, erythro
14	182	13.6	1856	2	B35049	ankyrin 1, erythro
15	182	13.6	1880	2	A35049	ankyrin - fruit fl
16	181.5	13.5	1549	2	T13940	hypothetical prote
17	176.5	13.2	2584	2	T24158	hypothetical prote
18	176.5	13.2	2606	2	T24157	hypothetical prote
19	175	13.0	495	2	T27995	probable potassium
20	173.5	12.9	888	2	D84650	ankyrin-repeat pro
21	173	12.9	333	2	JC7713	hypothetical prote
22	172.5	12.8	1188	2	T19552	2-5A-dependent RNA
23	171.5	12.8	741	2	A45771	hypothetical prote
24	171	12.8	1398	2	T21884	inv protein - mous
25	169.5	12.6	1062	2	T14151	ankyrin repeat pro
26	167	12.5	211	2	T18174	inversin - mouse
27	166.5	12.4	1062	2	T30255	protein phosphatas
28	166	12.4	658	2	S68418	serine/threonine-s
29	165.5	12.3	451	1	S68455	

30	164	12.2	642	2	S58154	hypothetical prote
31	163	12.2	118	2	A54412	V-1 protein - rat
32	163	12.2	319	2	A57291	cytokine inducible
33	163	12.2	439	2	JQ1729	ankyrin-repeat pro
34	163	12.2	1401	2	S11527	alpha-latrotoxin p
35	162	12.1	656	2	A34793	sex-determining pr
36	162	12.1	1004	2	A55142	myosin-light-chain
37	160	11.9	815	2	JG0197	hypothetical prote
38	159.5	11.9	1023	2	T26261	GA-binding protein
39	158.5	11.8	347	2	C40858	ankyrin-like prote
40	158.5	11.8	382	2	B40858	nuclear respirator
41	157.5	11.7	662	2	E84725	nuclear respirator
42	156.5	11.7	347	2	C48146	nuclear respirator
43	156.5	11.7	348	2	I38744	nuclear respirator
44	156.5	11.7	360	2	I38743	nuclear respirator
45	156.5	11.7	395	2	I38741	nuclear respirator

ALIGNMENTS

RESULT 1

AE2149  
hypothetical protein all12748 [imported] - Nostoc sp. (strain PCC 7120)  
C:Species: Nostoc sp.  
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
C:Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 30-Jun-2002  
C:Accession: AE2149  
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriyuch  
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S  
DNA Res. 8, 205-213, 2001  
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-Fixing Cyanobacterium An  
A:Reference number: AB1807; MUID:21595285; PMID:11759840  
A:Accession: AE2149  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-426 <KUR>  
A:Cross-references: GB:BA00019; PIDN:BA074447.1; PID:G17131841; GSPDB:GN00179  
A:Experimental source: strain PCC 7120  
C:Genetics:  
A:Gene: all12748

Query Match 16.4%; Score 219.5; DB 2; Length 426;  
Best Local Similarity 30.7%; Pred. No. 4.6e-10;  
Matches 62; Conservative 34; Mismatches 71; Indels 35; Gaps 4;

QY 62 QAGSSLKHSSTL-----TNROGNEVSALPATLDSLTHQLAAQGLDQLK 107  
DB 234 QDGSALHLATVEGYVDVQVLLNQGANTQIKKLGDTPLVVALQGH-----DQIV 285  
QY 108 EHLRK-----GDNLVNKPDERGFTPLWASAFGEIETVRFLLLEWGADPHLLAKRESAL 161  
DB 286 ETLKYGANVHGDNL-----GETPLTAAASQGHATATVRILLDYGANANIPASDGKTAL 338  
QY 162 SLASTGYTDIVGLLEERDVVDINIDYDNGGTPLLYAVRGNHVKCVREALARGADLTTEAD 221  
DB 339 IKATERNHFGVIOQLLAKGANVNYQDSVGATPILWASGGYNKVQIILEGGADTNLKNR 398  
QY 222 SGYTPMDLAVALLGYRKVQVIE 243  
DB 399 GGYTALMIAEFNGFRSIVQILK 420

RESULT 2

T15347  
ankyrin-related unc-44 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 02-Aug-2002  
C:Accession: T15347; T15346; T15344; T15345; A57282; B57282; C57282  
R:Gatung, S.  
submitted to the EMBL Data Library, February 1996  
A:Description: The sequence of C. elegans cosmid B0350.  
A:Reference number: Z18332

A/Accession: T15347  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-2039 <GAT>  
A/Cross-references: EMBL:U50071; NID:g1208871; PID:g1208873; PIDN:AAA93443.1  
A/Accession: T15346  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-1000, 'SKLQHT', 1002-1718, 'KWEELNRL', 1727, 'D', 'ES', 1942, 'PSPAQRS', 1950, 'IVA  
32, 'S', 2034-2035, 'GSPTRRSVEPEHRHSQHEDEGST' <GA2>  
A/Cross-references: EMBL:U50071; NID:g1208871; PID:g1208875; PIDN:AAA93445.1  
A/Accession: T15344  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-1718, 'KW', 1903-1905, 'NRLADESSPS', 1916-1917, 'QRSTIVAESTSEQVPE', 1934-1935, 'E  
<GA3>  
A/Cross-references: EMBL:U50071; NID:g1208871; PID:g1208874; PIDN:AAA93444.1  
A/Accession: T15345  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-1718, 'KWEELNRL', 1727, 'D', 'ES', 1942, 'PSPAQRS', 1950, 'IVAES', 1956-1957, 'EQVPE  
PTRRSVEPEHRHSQHEDEGST' <GA4>  
A/Cross-references: EMBL:U50071; NID:g1208871; PID:g1208876; PIDN:AAA93446.1  
R/Otsuka, A.J.; Franco, R.; Yang, B.; Shim, K.H.; Tang, L.Z.; Zhang, Y.Y.; Boontrakulpo  
J. Cell Biol. 129, 1081-1092, 1995  
A/Title: An ankyrin-related gene (unc-44) is necessary for proper axonal guidance in Cae  
A/Reference number: A57282; MUID:95263663; PMID:7744957  
A/Accession: A57282  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-852, 'GGG', 856-1000, 'SKLQHT', 1002-1319, 'IG', 1322-1595, 'DA', 1598-1718, 'KWE  
'SHRED', 2007-2008, 'TI', 2011, 2017, 'TT', 2020-2022, 'SHIS' <OTS>  
A/Cross-references: GB:U21734; NID:g790607; PIDN:AAA85854.1; PID:g790608  
A/Accession: B57282  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 831-852, 'GGG', 856-1319, 'IG', 1322-1595, 'DA', 1598-1718, 'KWEELNRL', 1727, 1799, 'E  
V', 1945-1947, 'VT', 1950, 'SH', 1975, 'SESP', 1980-1981, 'SPTRRSVEPEHRHS', 1984-1985, 'EDHEGS', 1  
A/Cross-references: GB:U21731  
A/Accession: C57282  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 194, 'F', 196, 'I', 198, 'DC', 201, 'G', 409, 'AV', 412, 'Q', 414, 824, 'S', 826, 'ER', 829, '4  
'TIV', 1828, 'ESTS', 1833, 'QV', 1836, 'E', 1934-1935, 'EQS', 1939, 'ESES', 1944, 'REDDGTIVTT', 194  
A/Cross-references: GB:U21732; NID:g790603; PIDN:AAA85853.1; PID:g790604  
C/Genetics:  
A/Gene: CESP:unc-44  
A/Introns: 97/3; 262/2; 535/1; 749/1; 786/3; 883/3; 1001/2; 1045/3; 1660/1; 1719/2; 1979  
C/Superfamily: ankyrin; ankyrin repeat homology  
F:164-192/Domain: ankyrin repeat homology <AN04>  
F:358-390/Domain: ankyrin repeat homology <AN1>  
F:391-423/Domain: ankyrin repeat homology <AN11>  
Query Match 16.0%; Score 214; DB 2; Length 2039;  
Best Local Similarity 27.3%; Pred. No. 1.2e-08;  
Matches 62; Conservative 36; Mismatches 87; Indels 42; Gaps 4;  
QY 19 SELGDPEDGEEAADGSDTVLFLPCTPEPVNPEPDASVSSPQAGSSLKHSSTLTNRQR 78  
DB 2 SNEGDPPOQOQPPESQEVQA---PAPEPGRAE----- 32  
QY 79 GNEVSALPATLDSLHQAQGLDQLKEHLRKCDNLVKNPDERGFTPLWASAFGEIE 138  
DB 33 -----GSASFRLARAGDLEKVELLRAGTD-INTSNANGLNSLHLSKEGHS 80  
QY 139 TVRFLLEWGADPHILAKERESALSLASTGYTDIVGLLERVDVINIYWNNGTPLLAV 198  
DB 81 VRELKROAQVDAATRKNTALHIASLAGOSLITVILVENGANVNVQSVNGFTPLVMAA 140  
QY 199 RGNHVKCEVALLARGADLTTEADSGYTPMDLAVALGY-RKVQVIEEN 244  
DB 141 QENHHEVVKYLKKGANQALSTEDGFTPLVALQCGHDRVAVLLEN 187

RESULT 3  
T43458  
hypothetical protein DKFZp434F0621.1 - human  
C/Species: Homo sapiens (man)  
C/Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 21-Jan-2000  
C/Accession: T43458  
R/Blum, H.; Bauersachs, S.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.  
Submitted to the Protein Sequence Database, December 1999  
A/Reference number: Z22517  
A/Accession: T43458  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-1031 <AAA>  
A/Cross-references: EMBL:AL133620  
A/Experimental source: adult testis; clone DKFZp434F0621  
C/Genetics:  
A/Note: DKFZp434F0621.1

Query Match 15.5%; Score 207.5; DB 2; Length 1031;  
Best Local Similarity 34.5%; Pred. No. 1.5e-08;  
Matches 51; Conservative 34; Mismatches 60; Indels 3; Gaps 3;  
QY 100 QGELDQLKEHLRKCDNLVKNPDERGFTPLWASAFGEIETVRFLLEWGADPHILAKERES 159  
DB 81 EGHVHIVEELKCGVNLNHR-DMGWTALMWACYKGRTDVVELLSHGANSVSTGLQYSV 139  
QY 160 ALSLASTG-GYTDIVGLLERVDVINIYWNNGTPLLAVRGNHVKCEVALLARGADLT 218  
DB 140 YPIIWAAGRHADIVHLLQNGAKVNCSDKYGTPLVWAARKGHLECVKHLAMGADVDO 199  
QY 219 EADSGYTPMDLAVALGY-RKVQVIEEN 245  
DB 200 EGANSMTALIVAVKGYTQSVKEILKRN 227

RESULT 4  
S37431  
ankyrin 2, neuronal long splice form - human  
N/Alternate names: ankyrin B, 440K splice form; ankyrin-B; brain ankyrin; non-erythroid  
N/Contains: ankyrin 2, short form  
C/Species: Homo sapiens (man)  
C/Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 13-Aug-1999  
C/Accession: S37431; A39643; B39643; A40334; A49462; S14533; S14569  
R/Chan, W.  
submitted to the EMBL Data Library, September 1993  
A/Reference number: S37431  
A/Accession: S37431  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-3924 <CHA>  
A/Cross-references: EMBL:Z26634; NID:g406287; PIDN:CAA81387.1; PID:g406288  
R/Octo, E.; Kunimoto, M.; McLaughlin, T.; Bennett, V.  
J. Cell Biol. 114, 241-253, 1991  
A/Title: Isolation and characterization of cDNAs encoding human brain ankyrins reveal a  
A/Reference number: A39643; MUID:91302466; PMID:1830053  
A/Accession: A39643  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-2077 <OT1>  
A/Cross-references: GB:X56957  
A/Accession: B39643  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-1443, 3585-3924 <OTT>  
A/Cross-references: EMBL:X56958  
R/Tse, W.T.; Menninger, J.C.; Yang-Feng, T.L.; Franke, U.; Sahr, K.E.; Lux, S.E.; Ward,  
Genomics 10, 858-866, 1991  
A/Title: Isolation and chromosomal localization of a novel nonerythroid ankyrin gene.  
A/Reference number: A40334; MUID:92009921; PMID:1833308  
A/Accession: A40334  
A/Molecule type: DNA  
A/Residues: 463-474, 'PE', 477-495 <TSE>

A;Cross-references: GB:M37123; NID:g178647; PIDN:AAA62828.1; PID:g178648  
R;Chan, W.; Kordeli, E.; Bennett, V.  
J. Cell Biol. 123, 1463-1473, 1993  
A;Title: 440-kD ankryrinB: structure of the major developmentally regulated domain and se  
A;Reference number: A49462; MUID:94075409; PMID:8253844  
A;Accession: A49462  
A;Status: preliminary; nucleic acid sequence not shown  
A;Molecule type: mRNA  
A;Residues: 1-3924 <RES>  
A;Cross-references: EMBL:Z26634; NID:g406287; PIDN:CAA81387.1; PID:g406288  
C;Genetics:  
A;Gene: GDB:ANK2  
A;Cross-references: GDB:127607; OMIM:106410  
A;Map position: 4q25-4q27  
C;Superfamily: ankryrin; ankryrin repeat homology  
C;Keywords: alternative splicing  
F;2-3924/Product: ankryrin 2, long form #status predicted <MAT>  
F;2-1443,3585-3924/Product: ankryrin 2, short form #status predicted <MA2>  
F;63-95/Domain: ankryrin repeat homology <AN01>  
F;96-128/Domain: ankryrin repeat homology <AN02>  
F;129-161/Domain: ankryrin repeat homology <AN03>  
F;162-190/Domain: ankryrin repeat homology <AN04>  
F;191-223/Domain: ankryrin repeat homology <AN05>  
F;232-264/Domain: ankryrin repeat homology <AN06>  
F;265-297/Domain: ankryrin repeat homology <AN07>  
F;298-330/Domain: ankryrin repeat homology <AN08>  
F;331-363/Domain: ankryrin repeat homology <AN09>  
F;364-396/Domain: ankryrin repeat homology <AN10>  
F;397-429/Domain: ankryrin repeat homology <AN11>  
F;430-462/Domain: ankryrin repeat homology <AN12>  
F;463-495/Domain: ankryrin repeat homology <AN13>  
F;496-528/Domain: ankryrin repeat homology <AN14>  
F;529-561/Domain: ankryrin repeat homology <AN15>  
F;562-594/Domain: ankryrin repeat homology <AN16>  
F;595-627/Domain: ankryrin repeat homology <AN17>  
F;628-660/Domain: ankryrin repeat homology <AN18>  
F;661-693/Domain: ankryrin repeat homology <AN19>  
F;694-726/Domain: ankryrin repeat homology <AN20>  
F;727-759/Domain: ankryrin repeat homology <AN21>  
F;760-792/Domain: ankryrin repeat homology <AN22>  
F;793-825/Domain: ankryrin repeat homology <AN23>  
  
Query Match 15.1%; Score 202.5; DB 2; Length 3924;  
Best Local Similarity 29.3%; Pred. No. 2.6e-07;  
Matches 56; Conservative 43; Mismatches 81; Indels 11; Gaps 4;  
  
QY 55 DASVSSPQAGSSLSKSTLTNRQGNESVALPATLDSLSIHQLAAGELDQLKEHLRKGD 114  
DB 5 DAAQKS-DSGEKFNSSQRRKRPKSDSNA-----SFLRAARAGNLDKVEYTKGGI 55  
  
QY 115 NLVVKPDERGFTPLIMASAFGEIETVRFLLEWGDPHILAKERESALSLASTGYTDIVG 174  
DB 56 D-INTCNQNGLNALHLAAKEGHVGLVQELLGRGSSVDSATKKGNTALHIASLAGQAEVVK 114  
  
QY 175 LLERDVVDINITYDMNGCTPLLYAVRGNHVKCEALLARGADLTTEADSGYTPMDLAVALG 234  
DB 115 VLVKEGANINAQSQNGFTPLYMAAQENHIDVKKYLLENGANOSTATEDGFTPLAVALQOG 174  
  
QY 235 YRK-VQQVIEN 244  
DB 175 HNOAVAILLEN 185  
  
RESULT 5  
A55575  
Ankryrin 3, long splice form - human  
N;Alternate names: ankryrin G  
C;Species: Homo sapiens (man)  
C;Date: 03-Mar-1995 #sequence\_revision 03-Mar-1995 #text\_change 20-Sep-1999  
C;Accession: A55575  
R;Kordeli, E.; Lambert, S.; Bennett, V.  
J. Biol. Chem. 270, 2352-2359, 1995  
A;Title: Ankryrin-G. A new ankryrin gene with neural-specific isoforms localized at the ax

A;Reference number: A55575; MUID:95138209; PMID:7836469  
A;Accession: A55575  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-4377 <KOR>  
A;Cross-references: GB:U13616; NID:g608024; PIDN:AAA64834.1; PID:g608025  
C;Genetics:  
A;Gene: GDB:ANK3  
A;Cross-references: GDB:424503; OMIM:600465  
A;Map position: 10q21-10q21  
C;Superfamily: unassigned ankryrin repeat proteins; ankryrin repeat homology; EGF homology  
C;Keywords: alternative splicing; peripheral membrane protein  
F;73-105/Domain: ankryrin repeat homology <AN01>  
F;106-138/Domain: ankryrin repeat homology <AN02>  
F;139-171/Domain: ankryrin repeat homology <AN03>  
F;172-200/Domain: ankryrin repeat homology <AN04>  
F;201-233/Domain: ankryrin repeat homology <AN05>  
F;234-266/Domain: ankryrin repeat homology <AN06>  
F;267-299/Domain: ankryrin repeat homology <AN07>  
F;300-332/Domain: ankryrin repeat homology <AN08>  
F;333-365/Domain: ankryrin repeat homology <AN09>  
F;366-398/Domain: ankryrin repeat homology <AN10>  
F;399-431/Domain: ankryrin repeat homology <AN11>  
F;432-464/Domain: ankryrin repeat homology <AN12>  
F;465-497/Domain: ankryrin repeat homology <AN13>  
F;498-530/Domain: ankryrin repeat homology <AN14>  
F;531-563/Domain: ankryrin repeat homology <AN15>  
F;564-596/Domain: ankryrin repeat homology <AN16>  
F;597-629/Domain: ankryrin repeat homology <AN17>  
F;630-662/Domain: ankryrin repeat homology <AN18>  
F;663-695/Domain: ankryrin repeat homology <AN19>  
F;696-728/Domain: ankryrin repeat homology <AN20>  
F;729-761/Domain: ankryrin repeat homology <AN21>  
F;762-794/Domain: ankryrin repeat homology <AN22>  
F;795-827/Domain: ankryrin repeat homology <AN23>  
  
Query Match 14.4%; Score 193; DB 2; Length 4377;  
Best Local Similarity 28.1%; Pred. No. 1.8e-06;  
Matches 50; Conservative 43; Mismatches 75; Indels 10; Gaps 3;  
  
QY 68 KHSSTLTNRQGNESVALPATLDSLSIHQLAAGELDQLKEHLRKGDNLVKNPDERGFTP 127  
DB 27 KHRKRSRDRKKKSDANA-----SYLRAARAGHLEKALDYIKNGVD-INICNQNGLNA 77  
  
QY 128 LIWASAFGEIETVRFLLEWGDPHILAKERESALSLASTGYTDIVGLLEERVDVINYD 187  
DB 78 LHLASKEGHEVVESELLQREANVDATKKGNTALHIASLAGQAEVVKVLTNGANVNAQS 137  
  
QY 188 WNGCTPLLYAVRGNHVKCEALLARGADLTTEADSGYTPMDLAVALGY-RKVQVIEN 244  
DB 138 QNGFTPLYMAAQENHLEVVKFLLDNGASQSLATEDGFTPLAVALQOGHDQVSLLEN 195  
  
RESULT 6  
S30385  
G9a protein - human  
C;Species: Homo sapiens (man)  
C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 21-Jan-2000  
C;Accession: S30385  
R;Milner, C.M.; Campbell, R.D.  
Biochem. J. 290, 811-818, 1993  
A;Title: The G9a gene in the human major histocompatibility complex encodes a novel prot  
A;Reference number: S30385; MUID:93207535; PMID:8457211  
A;Accession: S30385  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-1001 <MIL>  
A;Cross-references: EMBL:X69838; NID:g287864; PIDN:CAA49491.1; PID:g287865  
C;Superfamily: unassigned ankryrin repeat proteins; ankryrin repeat homology; EGF homology  
F;641-673/Domain: ankryrin repeat homology <ANR>  
  
Query Match 14.1%; Score 189; DB 2; Length 1001;  
Best Local Similarity 35.3%; Pred. No. 4.6e-07;



Matches	49, Conservative	18, Mismatches	72, Indels	0, Gaps	0,
QY	91 SLSIHQLAQGGELDQKEHLRKGDNLVKNKPDERGFTPLIWASAFGEIETVRFLEWGADP	150			
Db	543 STCLHHAAKIGNLEWWSLLSTGQVDVNAQDSGGWTPIIWAAEKHIEIVIRMLLTREGADV	602			
QY	151 HILAKERESALSLASTGGTYDIVGILLERDV DINITYDWNGGTPLLYAVRGNHVKCEALL	210			
Db	603 TLTDNEENICLHWASFTGSAIAIEVLLNARCDLHAVNYHGDTPLHIARESYHDCVLLFL	662			
QY	211 ARGADLTTEADSGYTPMDL	229			
Db	663 SRGANPELRNKEGDTAWDL	681			

RESULT 7  
T42714  
ankyrin 3, splice form 2 - mouse  
C/Species: Mus musculus (house mouse)  
C/Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 04-Mar-2000  
C/Accession: T42714  
R/Peters, L.L.; John, K.M.; Lu, F.M.; Eicher, E.M.; Higgins, A.; Yialamas, M.; Turtzo, I.  
J. Cell Biol. 130, 313-330, 1995  
A/Title: Ank3 (epithelial ankyrin), a widely distributed new member of the ankyrin gene  
the repeat domain.  
A/Reference number: 222237; MUID:95340633; PMID:7615634  
A/Accession: T42714  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: mRNA  
A/Residues: 1-1765 <PEP>  
A/Cross-references: EMBL:L40632; NID:g710548; PID:g710551; PIDN:AAB01605.1  
A/Experimental source: strain C57BL/6J; kidney  
C/Genetics:  
A/Gene: Ank3  
A/Map position: 10  
A/Introns: 1587/1  
C/Superfamily: ankyrin; ankyrin repeat homology  
C/Keywords: alternative splicing

Query Match	14.1%;	Score 188.5;	DB 2;	Length 1765;
Best Local Similarity	25.5%;	Pred. No. 1.1e-06;		
Matches 62;	Conservative 43;	Mismatches 77;	Indels 61;	Gaps 6;

QY	62	QASSLKHSHTT-----LTNRÖRGNEVSALPEATLD---SLSI-----HQLAAQGE	102
Dd	503	QOGASPNAAATTSGYTPLHLAAREGHEDVAAF--LLDHGASLITTKGFPLHVAAKYGK	560
QY	103	LDOLKEHLRKGDNLVKNPD-----ERGFT	126
Dd	561	LEVASLLLLQSAS----PDAAGKSGLTPLHVAHAHYDNÖKVALLLLDQGASPMAAKNGYT	616
QY	127	PLIWASA FGEIETVRFLLEWGADPHILAKERESALS LASTGYTDIVGLLERDV DINIY	186
Dd	617	PLHIAAKNQMDIATS LLEYGADANAVTRCGIASVHLAAQE GHDVMWSLLSRNANVNLS	676
QY	187	DWNGSTPLL YAVRGNHV KVEAL LA RGADLTTEADSGYTPMDLAVALGYRK VÖVIENHI	246
Dd	677	NKSGLTPLHLAAQEDRVNVAEVLVNOGAHVDAQTKMGYTPLHVGHCHYGNIKIVNFLQHS	736
QY	247	LKL 249	
Dd	737	AKV 739	

RESULT 8  
T42715  
ankyrin 3, splice form 3 - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_\_change 04-Mar-2000  
C:Accession: T42715  
R:Peters, L.L.; John, K.M.; Lu, F.M.; Eichler, E.M.; Higgins, A.; Yialamas, M.; Turtzo, L.  
J. Cell Biol. 130, 313-330, 1995  
A:Title: Ank3 (epithelial ankyrin), a widely distributed new member of the ankyrin gene

the repeat domain.  
A/Reference number: Z22237; MUID:95340633; PMID:7615634  
A/Accession: T42715  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: mRNA  
A/Residues: 1-1940 <PET>  
A/Cross-references: EMBL:L40632; NID:g710548; PID:g710549; PIDN:AAB01604.1  
A/Experimental source: strain C57BL/6J; kidney  
C/Genetics:  
A/Gene: Ank3  
A/Map position: 10  
A/Introns: 834/1  
C/Superfamily: ankyrin; ankyrin repeat homology  
C/Keywords: alternative splicing

	Query Match	14.1%;	Score 188.5;	DB 2;	Length 1940;
	Best Local Similarity	25.5%;	Pred. No. 1.3e-06;		
	Matches 62;	Conservative 43;	Mismatches 77;	Indels 61;	Gaps 6;
QY	62 QAGSSLKHSST-----LTNRQRGNEVSALPATLD---SLSI-----HQLAAGE 102	:   :   :	:	:	:
Dd	503 QOGASPNAATTSGYTPLHLAREGHEDVAAF--LLDHGASLSITTKGFTPLHVAAKKYGK 560	:	:	:	:
QY	103 LDQLKEHLRKGDNLVNKPDP-----ERGFT 126	:   :	:	:	:
Dd	561 LEVASLLLOKSAS----PDAAGKSGLTPLHVAAHYNQKVALLLLDQGASPHAAKKNGYT 616	:	:	:	:
QY	127 PLIWASA FGEIETVRFLLEWGADPHILAKERESALSASTGCYTDIVGLLERDVINITY 186	:   :	:	:	:
Dd	617 PLHIAAKNQMDIATSLLEYGADANAVTRQGIASVHLAAQEGHVDMVSLLSRNANVLIS 676	:	:	:	:
QY	187 DMNNGTPLLVA VRGNHYKCVEALLARGADLTTEADSGYTPMDLVALGYRKYQQVIENHI 246	: :         :	:	:	:
Dd	677 NKSGLTPLHLA AQEDRVNVAEVLVNQGAHVDAQTKMGYTPLHVHGCHYGNIKI VNFLLQHS 736	:	:	:	:
QY	247 LKL 249	:			
Dd	737 AKV 739				

RESULT 9  
T42713  
ankyrin 3, splice form 1 - mouse  
C/Species: Mus musculus (house mouse)  
C/Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 04-Mar-2000  
C/Accession: T42713  
R/Peters, L.L.; John, K.M.; Lu, F.M.; Eicher, E.M.; Higgins, A.; Vialamas, M.; Turtzo, J.  
J. Cell Biol. 130, 313-330, 1995  
A/Title: Ank3 (epithelial ankyrin), a widely distributed new member of the ankyrin gene  
the repeat domain.  
A/Reference number: Z22237; MUID:95340633; PMID:7615634  
A/Accession: T42713  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: mRNA  
A/Residues: 1-1943 <PET>  
A/Cross-references: EMBL:L40632; NID:g710548; PID:g710550; PIDN:AAB01606.1  
A/Experimental source: strain C57BL/6J; kidney  
C/Genetics:  
A/Gene: Ank3  
A/Map position: 10  
A/Introns: 855/1  
C/Function:  
A/Description: supposed to play an important role in the polarized distribution of many  
A/Note: major kidney ankyrin  
C/Superfamily: ankyrin; ankyrin repeat homology  
C/Keywords: alternative splicing

```

Query Match          14.1%; Score 188.5; DB 2; Length 1943;
Best Local Similarity 25.5%; Pred. NO. 1.3e-06;
Matches 62; Conservative 43; Mismatches 77; Indels 61; Gaps 6;

QY 62 QAGSSLSKHSST-----LTNRORGNEVSALPATLD---SLSI-----HQLAAGE 102
   | | : | : | | | | | | | | | | | | | | | | | | | | | | | |

```

Db 503 QQGASPNNAATTSCTPLHLAREGHEDVAAF--LDDHGASLSITTKGFTPLHVAAKYCK 560  
QY 103 LDQLKEHLRKGDNLVKNPD-----ERGFT 126  
Db 561 LEVASLLIÖKSAS----PDAAGKSGLTPLHVAHYDNÖKVALLLDDGASPHAAKNGYT 616  
QY 127 PLIWASAFGEIETVRFLEWGDADPHILAKERESALSLASTGYTDIVGLLERDVINITY 186  
Db 617 PLHIAAKKNQMDIATSLLEYGADANAVTRÖGIASVHLAAÖEGHVDMSLLSRNANVNLIS 676  
QY 187 DWNGTPLLVAVRGNHVKCEVALLARGADLTTEADSGYTPMDLAVAGYRKVOÖVIENHI 246  
Db 677 NKSGLTPLHLAAÖEDRVNVAEVLVNOGAHVDAÖTKMGYTPLVHVGCHYGNIKIVNELLÖHS 736  
QY 247 LKL 249  
Db 737 AKV 739

RESULT 10  
T42716

ankyrin 3, splice form 4 - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 04-Mar-2000  
C;Accession: T42716  
J;Peters, L.L.; John, K.M.; Lu, F.M.; Eicher, E.M.; Higgins, A.; Yialamas, M.; Turtzo, I.  
J;Cell Biol. 130, 313-330, 1995  
A;Title: Ank3 (epithelial ankyrin), a widely distributed new member of the ankyrin gene  
the repeat domain.  
A;Reference number: Z22237; MUID:95340633; PMID:7615634  
A;Accession: T42716  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-1961 <PET>  
A;Cross-references: EMBL:L40632; NID:g710548; PID:g710552; PIDN:AAB01607.1  
A;Experimental source: strain C57BL/6J; kidney  
C;Genetics:  
A;Gene: Ank3  
A;Map position: 10  
C;Superfamily: ankyrin; ankyrin repeat homology  
C;Keywords: alternative splicing

Query Match 14.1%; Score 188.5; DB 2; Length 1961;  
Best Local Similarity 25.5%; Pred. No. 1.3e-06;  
Matches 62; Conservative 43; Mismatches 77; Indels 61; Gaps 6;  
QY 62 QAGSLKXSTT-----LTNRÖRGNEVSALPATLD--SLSI-----HQLAÖGE 102  
Db 503 QQGASPNNAATTSCTPLHLAREGHEDVAAF--LDDHGASLSITTKGFTPLHVAAKYCK 560  
QY 103 LDQLKEHLRKGDNLVKNPD-----ERGFT 126  
Db 561 LEVASLLIÖKSAS----PDAAGKSGLTPLHVAHYDNÖKVALLLDDGASPHAAKNGYT 616  
QY 127 PLIWASAFGEIETVRFLEWGDADPHILAKERESALSLASTGYTDIVGLLERDVINITY 186  
Db 617 PLHIAAKKNQMDIATSLLEYGADANAVTRÖGIASVHLAAÖEGHVDMSLLSRNANVNLIS 676  
QY 187 DWNGTPLLVAVRGNHVKCEVALLARGADLTTEADSGYTPMDLAVAGYRKVOÖVIENHI 246  
Db 677 NKSGLTPLHLAAÖEDRVNVAEVLVNOGAHVDAÖTKMGYTPLVHVGCHYGNIKIVNELLÖHS 736  
QY 247 LKL 249  
Db 737 AKV 739

RESULT 11  
Suhuk  
ankyrin 1, erythrocyte splice form 1 - human  
N;Alternate names: ankyrin 2.1, erythrocyte; ankyrin-R  
N;Contains: ankyrin 2.2  
C;Species: Homo sapiens (man)

C;Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 22-Jun-1999  
C;Accession: S08275; A33219; PC2220; A35443  
R;Lux, S.E.; John, K.M.; Bennett, V.  
Nature 344, 36-42, 1990  
A;Title: Analysis of cDNA for human erythrocyte ankyrin indicates a repeated structure  
A;Reference number: S08275; MUID:90158830; PMID:2137557  
A;Accession: S08275  
A;Molecule type: mRNA  
A;Residues: 1-1881 <LUI>  
A;Cross-references: EMBL:X16609; NID:g28701; PIDN:CAA34610.1; PID:g28702  
A;Accession: A33219  
A;Molecule type: protein  
A;Residues: 2-7, 'X', 9-17, 'X', 19-20, 'T', 22-30, 733-749, 'A', 751-753; 828-833, 'X', 835-855, 'X'  
X', 1367; 1383-1427; 1601-1630; 1686-1698, 'D', 1700; 1763-1772 <LUX>  
A;Note: 845-Arg and 1392-Thr were also found  
R;Hermann, J.; Barel, M.; Frade, R.  
Biochem. Biophys. Res. Commun. 204, 453-460, 1994  
A;Title: Human erythrocyte ankyrin, a cytoskeleton component, generates the p57 membrane  
A;Reference number: PC2220; MUID:95071348; PMID:7526850  
A;Accession: PC2220  
A;Molecule type: protein  
A;Residues: 910-929 <HER>  
R;Davis, L.H.; Bennett, V.  
J. Biol. Chem. 265, 10589-10596, 1990  
A;Title: Mapping the binding sites of human erythrocyte ankyrin for the anion exchanger  
A;Reference number: A35443; MUID:90285190; PMID:2141335  
A;Accession: A35443  
A;Molecule type: protein  
A;Residues: 'X', 5, 'X', 7-12; 403-417, 'X', 419-422, 'H', 424, 'LQ', 797-800, 'L', 802-814; 862-863  
C;Genetics:  
A;Gene: GDB:ANK1; ANK  
A;Cross-references: GDB:118737; OMIM:182900  
A;Map position: 8p11.2-8p11.2  
C;Superfamily: ankyrin; ankyrin repeat homology  
C;Keywords: alternative splicing; phosphoprotein  
F;2-1881/Product: ankyrin 1, erythrocyte form 1 #status predicted <MAT1>  
F;2-1512, 1675-1881/Product: ankyrin 2.2, erythrocyte #status predicted <MAT2>  
F;2-827/Domain: 89K #status predicted <DOM1>  
F;44-76/Domain: anion exchange protein binding  
F;77-109/Domain: ankyrin repeat homology <AN01>  
F;110-142/Domain: ankyrin repeat homology <AN02>  
F;143-171/Domain: ankyrin repeat homology <AN03>  
F;172-204/Domain: ankyrin repeat homology <AN04>  
F;205-237/Domain: ankyrin repeat homology <AN05>  
F;238-270/Domain: ankyrin repeat homology <AN06>  
F;271-303/Domain: ankyrin repeat homology <AN07>  
F;304-336/Domain: ankyrin repeat homology <AN08>  
F;337-369/Domain: ankyrin repeat homology <AN09>  
F;370-402/Domain: ankyrin repeat homology <AN10>  
F;403-435/Domain: ankyrin repeat homology <AN11>  
F;436-468/Domain: ankyrin repeat homology <AN12>  
F;469-501/Domain: ankyrin repeat homology <AN13>  
F;502-534/Domain: ankyrin repeat homology <AN14>  
F;535-567/Domain: ankyrin repeat homology <AN15>  
F;568-600/Domain: ankyrin repeat homology <AN16>  
F;601-633/Domain: ankyrin repeat homology <AN17>  
F;634-666/Domain: ankyrin repeat homology <AN18>  
F;667-699/Domain: ankyrin repeat homology <AN19>  
F;700-732/Domain: ankyrin repeat homology <AN20>  
F;733-765/Domain: ankyrin repeat homology <AN21>  
F;766-798/Domain: ankyrin repeat homology <AN22>  
F;828-1382/Domain: 62K #status predicted <DOM2>  
F;828-1382/Region: spectrin binding  
F;1383-1881/Domain: 55K #status predicted <DOM3>  
Query Match 13.7%; Score 184; DB 1; Length 1881;  
Best Local Similarity 23.1%; Pred. No. 2.9e-06;  
Matches 54; Conservative 37; Mismatches 69; Indels 74; Gaps 3;  
QY 74 TNÖRGNEVSALPATIDSLSIHQLAÖGELDQLKEHLRKGDNLVKNKPDGERGFTPLIWASA 133  
Db 73 TTTKGN-----TALHIALAGÖDEVRELTVNGAN--VNAÖSQÖKGFTPLWMAÖ 120





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C:Date: 17-Nov-1995 #sequence_revision 17-Nov-1995 #text_change 10-Jul-1998
C:Accession: B35049
R:Lambert, S.; Yu, H.; Prchal, J.T.; Lawler, J.; Ruff, P.; Speicher, D.; Cheung, M.C.; K
Proc. Natl. Acad. Sci. U.S.A. 87, 1730-1734, 1990
A:Title: cDNA sequence for human erythrocyte ankyrin.
A:Reference number: A35049; MUID:90175370; PMID:1689849
A:Accession: B35049
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1856 <LAM>
C:Genetics:
A:Gene: GDB:ANK1; ANK
A:Cross-references: GDB:118737; OMIM:182900
A:Map position: 8p11.2-8p11.2
C:Superfamily: ankyrin; ankyrin repeat homology
C:Keywords: alternative splicing
F:2-1856/Product: ankyrin 1, erythrocyte form 3 #status predicted <MAT>
F:2-1513,1676-1856/Product: ankyrin 2.2, erythrocyte #status predicted <MA2>
F:44-76/Domain: ankyrin repeat homology <AN01>
F:77-109/Domain: ankyrin repeat homology <AN02>
F:110-142/Domain: ankyrin repeat homology <AN03>
F:143-171/Domain: ankyrin repeat homology <AN04>
F:172-204/Domain: ankyrin repeat homology <AN05>
F:205-237/Domain: ankyrin repeat homology <AN06>
F:238-270/Domain: ankyrin repeat homology <AN07>
F:271-303/Domain: ankyrin repeat homology <AN08>
F:304-336/Domain: ankyrin repeat homology <AN09>
F:337-369/Domain: ankyrin repeat homology <AN10>
F:370-402/Domain: ankyrin repeat homology <AN11>
F:403-435/Domain: ankyrin repeat homology <AN12>
F:436-468/Domain: ankyrin repeat homology <AN13>
F:469-501/Domain: ankyrin repeat homology <AN14>
F:502-534/Domain: ankyrin repeat homology <AN15>
F:535-567/Domain: ankyrin repeat homology <AN16>
F:568-600/Domain: ankyrin repeat homology <AN17>
F:601-633/Domain: ankyrin repeat homology <AN18>
F:634-666/Domain: ankyrin repeat homology <AN19>
F:667-699/Domain: ankyrin repeat homology <AN20>
F:700-732/Domain: ankyrin repeat homology <AN21>
F:733-765/Domain: ankyrin repeat homology <AN22>
F:766-798/Domain: ankyrin repeat homology <AN23>

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RESULT 15  
A35049  
ankyrrin 1, erythrocyte splice form 2 - human  
N/Alternate names: ankyrrin 2.1, erythrocyte; ankyrrin-R  
N/Contains: ankyrrin 2.2, erythrocyte  
C/Species: Homo sapiens (man)  
C/Date: 27-Jul-1990 #sequence\_revision 01-Oct-1992 #text\_change 04-Sep-1998  
C/Accession: A35049  
R/Lambert, S.; Yu, H.; Prchal, J.T.; Lawler, J.; Ruff, P.; Speicher, D.; Cheung, M.C.; K  
Proc. Natl. Acad. Sci. U.S.A. 87, 1730-1734, 1990

A;Title: cDNA sequence for human erythrocyte ankyrin.  
A;Reference number: A35049; MUID:90175370; PMID:1689849  
A;Accession: A35049  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-1880 <LAM>  
A;Cross-references: GB:M28880  
C;Genetics:  
A;Gene: GDB:ANK1; ANK  
A;Cross-references: GDB:118737; OMIM:182900  
A;Map position: 8p11.2-8p11.2  
C;Superfamily: ankyrin; ankyrin repeat homology  
C;Keywords: alternative splicing; cytoskeleton  
F;2-1880/Product: ankyrin 1, erythrocyte form 2 #status predicted <MAT>  
F;2-1513,1676-1880/Product: ankyrin 2.2, erythrocyte #status predicted <MA2>  
F;44-76/Domain: ankyrin repeat homology <AN01>  
F;77-109/Domain: ankyrin repeat homology <AN02>  
F;110-142/Domain: ankyrin repeat homology <AN03>  
F;143-171/Domain: ankyrin repeat homology <AN04>  
F;172-204/Domain: ankyrin repeat homology <AN05>  
F;205-237/Domain: ankyrin repeat homology <AN06>  
F;238-270/Domain: ankyrin repeat homology <AN07>  
F;271-303/Domain: ankyrin repeat homology <AN08>  
F;304-336/Domain: ankyrin repeat homology <AN09>  
F;337-369/Domain: ankyrin repeat homology <AN10>  
F;370-402/Domain: ankyrin repeat homology <AN11>  
F;403-435/Domain: ankyrin repeat homology <AN12>  
F;436-468/Domain: ankyrin repeat homology <AN13>  
F;469-501/Domain: ankyrin repeat homology <AN14>  
F;502-534/Domain: ankyrin repeat homology <AN15>  
F;535-567/Domain: ankyrin repeat homology <AN16>  
F;568-600/Domain: ankyrin repeat homology <AN17>  
F;601-633/Domain: ankyrin repeat homology <AN18>  
F;634-666/Domain: ankyrin repeat homology <AN19>  
F;667-699/Domain: ankyrin repeat homology <AN20>  
F;700-732/Domain: ankyrin repeat homology <AN21>  
F;733-765/Domain: ankyrin repeat homology <AN22>  
F;766-798/Domain: ankyrin repeat homology <AN23>

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Query Match      13.6%; Score 182; DB 2; Length 1880;
Best Local Similarity 26.4%; Pred. No. 4.2e-06;
Matches 61; Conservative 34; Mismatches 135; Indels 1; Gaps 1;

QY    8 EDLIQTQOTPASELGDPEDGEEAADGSDTVVLSLPCTDEPVNPEPDASVSSPQAGSSL 67
      ::||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db    421 KNLLQRGASPNSNVKVFETPLHMAARAGHTEVAKYLLQNKAKNNAKAKDDQTPHCAARI 480

QY    68 KHSTTLTNRQGENEVSALPATLDSLISHLAAQGELDQLKEHLRKGDNLVNKPDERGFPT 127
      ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db    481 GHTNMVKLLLENNANPNLATTTAGHTPLHIAAREGHVEIVALLLEKEASQACM-TKKGFTF 539

QY    128 LIWASA FGEIETVRFLLEMGA DPHILAKERESALS LASTGGYTDIVGLLERVDVINITYD 187
       |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db    540 LHVAAKYGVKRVVAELLERDAHPNAAGKNGLTPLHVAAYHNHNDLIVKLLPRGSGSPHSPA 599

QY    188 WNGGTPLL YAVRGNHVVCYEALLARGADLTTEADSGYTPMDLAVALGYRKV 238
       |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db    600 WNGYTPLHIAAKONQVEVARSLLYQGSANAESVGVTPLHLAAQEGHAEM 650

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Search completed: March 17, 2003, 16:41:10  
Job time : 27 secs

